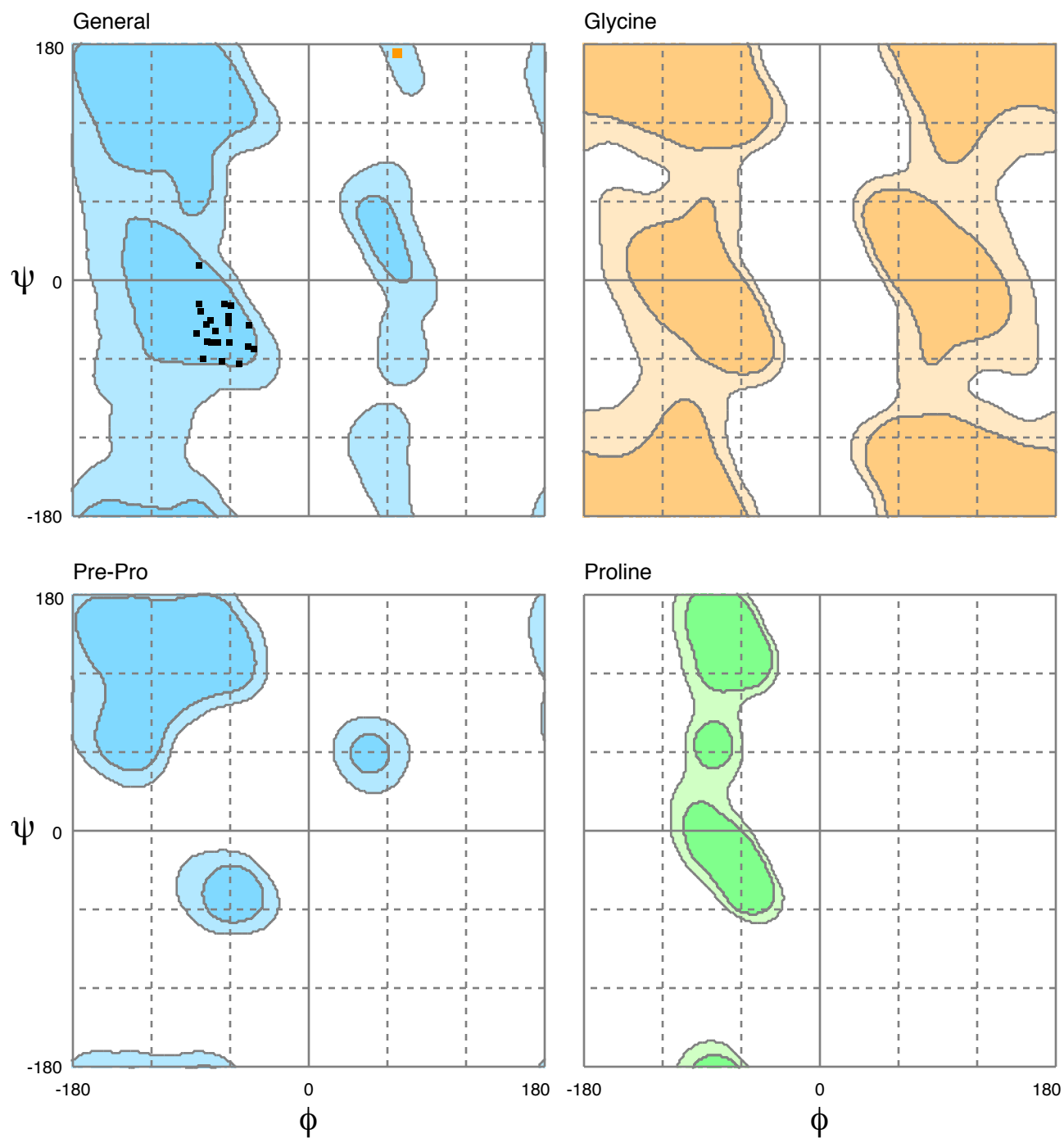


Number of residues in favoured region (~98.0% expected) : 22 (95.7%)  
 Number of residues in allowed region (~2.0% expected) : 1 (4.3%)  
 Number of residues in outlier region : 0 (0.0%)

RAMPAGE by Paul de Bakker and Simon Lovell available at <http://www-cryst.bioc.cam.ac.uk/rampage/>

Please cite: S.C. Lovell, I.W. Davis, W.B. Arendall III, P.I.W. de Bakker, J.M. Word, M.G. Prisant, J.S. Richardson & D.C. Richardson (2002)  
 Structure validation by  $\alpha$  geometry:  $\phi/\psi$  and  $C\beta$  deviation. *Proteins: Structure, Function & Genetics*. **50**: 437-450



	General Favoured		General Allowed
	Glycine Favoured		Glycine Allowed
	Pre-Pro Favoured		Pre-Pro Allowed
	Proline Favoured		Proline Allowed

Number of residues in favoured region (~98.0% expected) : 22 (95.7%)  
 Number of residues in allowed region (~2.0% expected) : 1 (4.3%)  
 Number of residues in outlier region : 0 (0.0%)

RAMPAGE by Paul de Bakker and Simon Lovell available at <http://www-cryst.bioc.cam.ac.uk/rampage/>

Please cite: S.C. Lovell, I.W. Davis, W.B. Arendall III, P.I.W. de Bakker, J.M. Word, M.G. Prisant, J.S. Richardson & D.C. Richardson (2002)  
 Structure validation by  $\alpha$  geometry:  $\phi/\psi$  and  $C\beta$  deviation. *Proteins: Structure, Function & Genetics*. **50**: 437-450